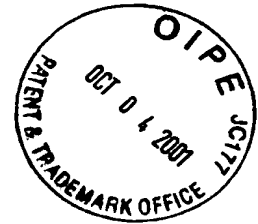


#6



SEQUENCE LISTING

<110> NOVIMMUNE SA

<120> NEW TRANSCRIPTION FACTOR OF MHC CLASS II GENES,
SUBSTANCES CAPABLE OF INHIBITING THIS NEW TRANSCRIPTION
FACTOR AND MEDICAL USES OF THESE SUBSTANCES

<130> B3991AB-CS/KR

<140> US/09/840,243

<141> 2001-04-24

<150> 98120085.0

<151> 1998-10-24

<160> 19

<170> PatentIn Ver. 2.1

<210> 1

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

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ccgtacgcgt ctagaccatg gagcttacct agcctgcaga 40

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<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 2

ttcgaattct cgagtgtctg agtccccggc a 31

<210> 3

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 3

ccgtacgcgt ctagaccatg gagccactc aggttgc 37

<210> 4

<211> 32

<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

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<210> 5
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

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ccagctctag actccaccac tctcaccaac 30

<210> 6
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<212> DNA
<213> Artificial Sequence

<220>
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ccttcgaatt ctcgctcttt tgccaggatg 30

<210> 7
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<220>
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ggttctctag attggcagca ctgggggatag 30

<210> 8
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<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

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gctacgaatt ccagcagaca cagccaaaac 30

<210> 9
<211> 69
<212> DNA
<213> Artificial Sequence

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<223> Description of Artificial Sequence:primer

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gcagaagac 69

<210> 10

<211> 1345

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (418)..(1200)

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cttttccttg agagacgagt tgggggagtc ctccacgcat taccactcg ggccgcaaaa 180
actcccttct ttagccctct gccccgccc ttgcttataa gcctttgaga ccgcagaagg 240
gaccttggtg tggaacggga cggccaagag gaagccagat cgctgagggg ccggtctcca 300
gtttgcctcc tgctatatcc attggaagag aaaagtttgt gacttggggc cccaagtttt 360
gagagaactg ggctttcggc gcggggggac agaggaggct cgtggggagc tttcccc 417
atg gag ctt acc cag cct gca gaa gac ctc atc cag acc cag cag acc 465
Met Glu Leu Thr Gln Pro Ala Glu Asp Leu Ile Gln Thr Gln Gln Thr
1 5 10 15
cct gcc tca gaa ctt ggg gac cct gaa gac ccc gga gag gag gct gca 513
Pro Ala Ser Glu Leu Gly Asp Pro Glu Asp Pro Gly Glu Glu Ala Ala
20 25 30
gat ggc tca gac act gtg gtc ctc agt ctc ttt ccc tgc acc cct gag 561
Asp Gly Ser Asp Thr Val Val Leu Ser Leu Phe Pro Cys Thr Pro Glu
35 40 45
cct gtg aat cct gaa ccg gat gcc agt gtt tcc tct cca cag gca ggc 609
Pro Val Asn Pro Glu Pro Asp Ala Ser Val Ser Ser Pro Gln Ala Gly
50 55 60
agc tcc ctg aag cac tcc acc act ctc acc aac cgg cag cga ggg aac 657
Ser Ser Leu Lys His Ser Thr Thr Leu Thr Asn Arg Gln Arg Gly Asn
65 70 75 80
gag gtg tca gct ctg ccg gcc acc cta gac tcc ctg tcc atc cac cag 705
Glu Val Ser Ala Leu Pro Ala Thr Leu Asp Ser Leu Ser Ile His Gln
85 90 95
ctc gca gca cag ggg gag ctg gac cag ctg aag gag cat ttg cgg aaa 753
Leu Ala Ala Gln Gly Glu Leu Asp Gln Leu Lys Glu His Leu Arg Lys
100 105 110
ggg gac aac ctc gtc aac aag cca gac gag cgc ggc ttc acc ccc ctc 801

Gly	Asp	Asn	Leu	Val	Asn	Lys	Pro	Asp	Glu	Arg	Gly	Phe	Thr	Pro	Leu		
		115					120					125					
atc	tgg	gcc	tcc	gcc	ttt	gga	gag	att	gag	acc	gtt	cgc	ttc	ctg	ctg	849	
Ile	Trp	Ala	Ser	Ala	Phe	Gly	Glu	Ile	Glu	Thr	Val	Arg	Phe	Leu	Leu		
	130					135					140						
gag	tgg	ggt	gcc	gac	ccc	cac	atc	ctg	gca	aaa	gag	cga	gag	agc	gcc	897	
Glu	Trp	Gly	Ala	Asp	Pro	His	Ile	Leu	Ala	Lys	Glu	Arg	Glu	Ser	Ala		
	145				150					155					160		
ctg	tgc	ctg	gcc	agc	aca	ggc	ggc	tac	aca	gac	att	gtg	ggg	ctg	ctg	945	
Leu	Ser	Leu	Ala	Ser	Thr	Gly	Gly	Tyr	Thr	Asp	Ile	Val	Gly	Leu	Leu		
				165					170					175			
ctg	gag	cgt	gac	gtg	gac	atc	aac	atc	tat	gat	tgg	aat	gga	ggg	acg	993	
Leu	Glu	Arg	Asp	Val	Asp	Ile	Asn	Ile	Tyr	Asp	Trp	Asn	Gly	Gly	Thr		
			180					185					190				
cca	ctg	ctg	tac	gct	gtg	cgc	ggg	aac	cac	gtg	aaa	tgc	gtt	gag	gcc	1041	
Pro	Leu	Leu	Tyr	Ala	Val	Arg	Gly	Asn	His	Val	Lys	Cys	Val	Glu	Ala		
			195				200					205					
ttg	ctg	gcc	cga	ggc	gct	gac	ctc	acc	acc	gaa	gcc	gac	tct	ggc	tac	1089	
Leu	Leu	Ala	Arg	Gly	Ala	Asp	Leu	Thr	Thr	Glu	Ala	Asp	Ser	Gly	Tyr		
	210					215					220						
acc	ccg	atg	gac	ctt	gcc	gtg	gcc	ctg	gga	tac	cgg	aaa	gtg	caa	cag	1137	
Thr	Pro	Met	Asp	Leu	Ala	Val	Ala	Leu	Gly	Tyr	Arg	Lys	Val	Gln	Gln		
	225				230				235					240			
gtg	atc	gag	aac	cac	atc	ctc	aag	ctc	ttc	cag	agc	aac	ctg	gtg	ccc	1185	
Val	Ile	Glu	Asn	His	Ile	Leu	Lys	Leu	Phe	Gln	Ser	Asn	Leu	Val	Pro		
				245					250					255			
gct	gac	cct	gag	tga	aggccgcctg	ccgggggactc	agacactcag	ggaacaaaat								1240	
Ala	Asp	Pro	Glu														
			260														
ggtcagccag	agctgggggaa	accacagaact	gacttcaaag	gcagcttctg	gacagggtggt											1300	
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<210> 11
 <211> 260
 <212> PRT
 <213> Homo sapiens

<400> 11
 Met Glu Leu Thr Gln Pro Ala Glu Asp Leu Ile Gln Thr Gln Gln Thr
 1 5 10 15
 Pro Ala Ser Glu Leu Gly Asp Pro Glu Asp Pro Gly Glu Glu Ala Ala
 20 25 30
 Asp Gly Ser Asp Thr Val Val Leu Ser Leu Phe Pro Cys Thr Pro Glu
 35 40 45
 Pro Val Asn Pro Glu Pro Asp Ala Ser Val Ser Ser Pro Gln Ala Gly
 50 55 60

Ser Ser Leu Lys His Ser Thr Thr Leu Thr Asn Arg Gln Arg Gly Asn
 65 70 75 80
 Glu Val Ser Ala Leu Pro Ala Thr Leu Asp Ser Leu Ser Ile His Gln
 85 90 95
 Leu Ala Ala Gln Gly Glu Leu Asp Gln Leu Lys Glu His Leu Arg Lys
 100 105 110
 Gly Asp Asn Leu Val Asn Lys Pro Asp Glu Arg Gly Phe Thr Pro Leu
 115 120 125
 Ile Trp Ala Ser Ala Phe Gly Glu Ile Glu Thr Val Arg Phe Leu Leu
 130 135 140
 Glu Trp Gly Ala Asp Pro His Ile Leu Ala Lys Glu Arg Glu Ser Ala
 145 150 155 160
 Leu Ser Leu Ala Ser Thr Gly Gly Tyr Thr Asp Ile Val Gly Leu Leu
 165 170 175
 Leu Glu Arg Asp Val Asp Ile Asn Ile Tyr Asp Trp Asn Gly Gly Thr
 180 185 190
 Pro Leu Leu Tyr Ala Val Arg Gly Asn His Val Lys Cys Val Glu Ala
 195 200 205
 Leu Leu Ala Arg Gly Ala Asp Leu Thr Thr Glu Ala Asp Ser Gly Tyr
 210 215 220
 Thr Pro Met Asp Leu Ala Val Ala Leu Gly Tyr Arg Lys Val Gln Gln
 225 230 235 240
 Val Ile Glu Asn His Ile Leu Lys Leu Phe Gln Ser Asn Leu Val Pro
 245 250 255
 Ala Asp Pro Glu
 260

<210> 12
 <211> 260
 <212> PRT
 <213> Homo sapiens

<400> 12
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 Pro Ala Ser Glu Leu Gly Asp Pro Glu Asp Pro Gly Glu Glu Ala Ala
 20 25 30
 Asp Gly Ser Asp Thr Val Val Leu Ser Leu Phe Pro Cys Thr Pro Glu
 35 40 45

Pro Val Asn Pro Glu Pro Asp Ala Ser Val Ser Ser Pro Gln Ala Gly
 50 55 60
 Ser Ser Leu Lys His Ser Thr Thr Leu Thr Asn Arg Gln Arg Gly Asn
 65 70 75 80
 Glu Val Ser Ala Leu Pro Ala Thr Leu Asp Ser Leu Ser Ile His Gln
 85 90 95
 Leu Ala Ala Gln Gly Glu Leu Asp Gln Leu Lys Glu His Leu Arg Lys
 100 105 110
 Gly Asp Asn Leu Val Asn Lys Pro Asp Glu Arg Gly Phe Thr Pro Leu
 115 120 125
 Ile Trp Ala Ser Ala Phe Gly Glu Ile Glu Thr Val Arg Phe Leu Leu
 130 135 140
 Glu Trp Gly Ala Asp Pro His Ile Leu Ala Lys Glu Arg Glu Ser Ala
 145 150 155 160
 Leu Ser Leu Ala Ser Thr Gly Gly Tyr Thr Asp Ile Val Gly Leu Leu
 165 170 175
 Leu Glu Arg Asp Val Asp Ile Asn Ile Tyr Asp Trp Asn Gly Gly Thr
 180 185 190
 Pro Leu Leu Tyr Ala Val Arg Gly Asn His Val Lys Cys Val Glu Ala
 195 200 205
 Leu Leu Ala Arg Gly Ala Asp Leu Thr Thr Glu Ala Asp Ser Gly Tyr
 210 215 220
 Thr Pro Met Asp Leu Ala Val Ala Leu Gly Tyr Arg Lys Val Gln Gln
 225 230 235 240
 Val Ile Glu Asn His Ile Leu Lys Leu Phe Gln Ser Asn Leu Val Pro
 245 250 255
 Ala Asp Pro Glu
 260

<210> 13
 <211> 269
 <212> PRT
 <213> Murinae gen. sp.

<400> 13
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 Pro Val Pro Asp Leu Glu Asp Pro Glu Asp Thr Arg Asp Glu Ser Pro
 20 25 30
 Glu Asn Ser Asp Thr Val Val Leu Ser Leu Phe Pro Cys Thr Pro Asp
 35 40 45
 Ala Val Asn Pro Glu Ala Asp Ala Ser Ala Ser Ser Leu Gln Gly Ser
 50 55 60

Phe Leu Lys His Ser Thr Thr Leu Thr Asn Arg Gln Arg Gly Asn Glu
 65 70 75 80
 Val Ser Ala Leu Pro Ala Thr Leu Asp Ser Leu Ser Ile His Gln Leu
 85 90 95
 Ala Ala Gln Gly Glu Leu Ser Gln Leu Lys Asp His Leu Arg Lys Gly
 100 105 110
 Ala Cys Pro Ala Cys Thr Cys Leu Ser Gly Asn Asn Leu Ile Asn Lys
 115 120 125
 Pro Asp Glu Arg Gly Phe Thr Pro Leu Ile Trp Ala Ser Ala Phe Gly
 130 135 140
 Glu Ile Glu Thr Val Arg Phe Leu Leu Asp Trp Gly Ala Asp Pro His
 145 150 155 160
 Ile Leu Ala Lys Glu Arg Glu Ser Ala Leu Ser Leu Ala Ser Met Gly
 165 170 175
 Gly Tyr Thr Asp Ile Val Arg Leu Leu Leu Asp Arg Asp Val Asp Ile
 180 185 190
 Asn Ile Tyr Asp Trp Asn Gly Gly Thr Pro Leu Leu Tyr Ala Val Arg
 195 200 205
 Gly Asn His Val Lys Cys Val Glu Ala Leu Leu Ala Arg Gly Ala Asp
 210 215 220
 Leu Thr Thr Glu Ala Asp Ser Gly Tyr Thr Pro Met Asp Leu Ala Val
 225 230 235 240
 Ala Leu Gly Tyr Arg Lys Val Gln Gln Val Met Glu Ser His Ile Leu
 245 250 255
 Arg Leu Phe Gln Ser Thr Leu Gly Pro Val Asp Pro Glu
 260 265

<210> 14
 <211> 111
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(111)

<400> 14
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 Thr Leu Asp Trp Cys Arg Pro Pro His Pro Gly Lys Arg Ala Arg Glu
 1 5 10 15
 cgc cct gtc gct ggc cag cac agg cgg cta cac aga cat tgt ggg gct 96
 Arg Pro Val Ala Gly Gln His Arg Arg Leu His Arg His Cys Gly Ala
 20 25 30
 gct gct gga gcg tga 111
 Ala Ala Gly Ala

35

<210> 15
<211> 36
<212> PRT
<213> Homo sapiens

<400> 15
Thr Leu Asp Trp Cys Arg Pro Pro His Pro Gly Lys Arg Ala Arg Glu
1 5 10 15

Arg Pro Val Ala Gly Gln His Arg Arg Leu His Arg His Cys Gly Ala
20 25 30

Ala Ala Gly Ala
35

<210> 16
<211> 42
<212> DNA
<213> Homo sapiens

<220>
<221> exon
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ctggtggtat tgcccgcctc ctctgccag gtg aca acc tcg 42

<210> 17
<211> 74
<212> DNA
<213> Homo sapiens

<220>
<221> exon
<222> (1)..(27)

<400> 17
gag acc gtt cgc ttc ctg ctg gag tgg gtgcgtccca gccagctgg 47
gcagctgggg gggtcccggg ggcctta 74

<210> 18
<211> 220
<212> PRT
<213> Homo sapiens

<220>
<221> UNSURE
<222> 31

<220>
<221> UNSURE
<222> 148

<220>

<221> UNSURE

<222> 159

<400> 18

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Ile His Thr Ser Pro Ser Pro Gly Ile Gln Val Arg His Val Xaa Thr
20 25 30
Pro Ser Thr Thr Lys His Phe Ser Pro Ile Lys Gln Ser Thr Thr Leu
35 40 45
Thr Asn Lys His Arg Gly Asn Glu Val Ser Thr Thr Pro Leu Leu Ala
50 55 60
Asn Ser Leu Ser Val His Gln Leu Ala Ala Gln Gly Glu Met Leu Tyr
65 70 75 80
Leu Ala Thr Arg Ile Glu Gln Glu Asn Val Ile Asn His Thr Asp Glu
85 90 95
Glu Gly Phe Thr Pro Leu Met Trp Ala Ala Ala His Gly Gln Ile Ala
100 105 110
Val Val Glu Phe Leu Leu Gln Asn Gly Ala Asp Pro Gln Leu Leu Gly
115 120 125
Lys Gly Arg Glu Ser Ala Leu Ser Leu Ala Cys Ser Lys Gly Tyr Thr
130 135 140
Asp Ile Val Xaa Met Leu Leu Asp Cys Gly Val Asp Val Asn Xaa Tyr
145 150 155 160
Asp Trp Asn Gly Gly Thr Pro Leu Leu Tyr Ala Val His Gly Asn His
165 170 175
Val Lys Cys Val Lys Met Leu Leu Glu Ser Gly Ala Asp Pro Thr Ile
180 185 190
Glu Thr Asp Ser Gly Tyr Asn Ser Met Asp Leu Ala Val Ala Leu Gly
195 200 205
Ile Glu Val Phe Asn Arg Leu Leu Ser His Ile Cys
210 215 220

<210> 19

<211> 218

<212> PRT

<213> Murinae gen. sp.

<400> 19

Ala Ser Val Leu Phe Lys Ala Glu Cys Asn Ile His Thr Ser Pro Ser
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Pro Gly Ile Gln Val Arg His Val Tyr Thr Pro Ser Thr Thr Lys His
20 25 30
Phe Ser Pro Ile Lys Gln Ser Thr Thr Leu Thr Asn Lys His Arg Gly
35 40 45

Asn Glu Val Ser Thr Thr Pro Leu Leu Ala Asn Ser Leu Ser Ala His
 50 55 60
 Gln Leu Ala Ala Gln Gly Glu Met Leu Tyr Leu Ala Thr Arg Ile Glu
 65 70 75 80
 Gln Glu Asn Val Ile Asn His Thr Asp Glu Glu Gly Phe Thr Pro Leu
 85 90 95
 Met Trp Ala Ala Ala His Gly Gln Ile Ala Val Val Glu Phe Leu Leu
 100 105 110
 Gln Asn Gly Ala Asp Pro Gln Leu Leu Gly Lys Gly Arg Glu Ser Ala
 115 120 125
 Leu Ser Leu Ala Cys Ser Lys Gly Tyr Thr Asp Ile Val Lys Met Leu
 130 135 140
 Leu Asp Cys Gly Val Asp Val Asn Glu Tyr Asp Trp Asn Gly Gly Thr
 145 150 155 160
 Pro Leu Leu Tyr Ala Gly His Gly Asn His Val Lys Cys Val Lys Met
 165 170 175
 Leu Leu Glu Asn Gly Ala Asp Pro Thr Ile Glu Thr Asp Ser Gly Tyr
 180 185 190
 Asn Ser Met Asp Leu Ala Val Ala Leu Gly Ile Glu Gly Cys Ser Asp
 195 200 205
 Tyr Met Leu Val Thr Asp Val Phe Arg Ile
 210 215